AMENDMENTS TO THE CLAIMS:

The following listing of claims replaces all prior listings, and all prior versions, of claims in the application.

LISTING OF CLAIMS:

1-5. (Cancelled).

6. (Withdrawn) A kit for gene expression analysis comprising:

a probe comprising a sequence identical or complementary to a first base sequence, and labeled at one end with a fluorophore and at another end with a quencher, and a primer comprising a sequence identical to a second base sequence and bound to a position closer to the 5' end than the first base sequence,

wherein the first base sequence and the second base sequence are nonspecific to a base sequence of a target gene and are introduced into the target gene.

7. (Withdrawn) The kit according to claim 6, wherein each of the two or more types of probes comprises several module sequences of 3 or 4 bases, the both terminal bases of each module sequence are identical to each other, and each probe is constituted by rearranging the order of module sequences having the identical terminal bases.

8. (New) A method for gene expression analysis comprising:

preparing first nucleotides including a targeted gene by using a first sample and introducing a first base sequence and a second base sequence, which are nonspecific to the base sequence of the targeted gene, to the targeted gene so that

the second base sequence is bound to a position closer to the 5' end than is the first base sequence,

preparing second nucleotides including the targeted gene by using a second sample and introducing a third base sequence and the second base sequence, which are nonspecific to the base sequence of the targeted gene, to the targeted gene so that the second base sequence is bound to a position closer to the 5' end than is the third base sequence,

subjecting the first nucleotides and the second nucleotides to nucleic acid amplification using a primer comprising a base sequence specifically hybridizing to the targeted gene, a primer comprising a base sequence identical to the second base sequence, a first probe comprising a base sequence identical orf complementary to the first base sequence, and labeled at one end with a first fluorophore and at another end with a quencher, a second probe comprising a base sequence identical or complementary to the third base sequence, and labeled at one end with a second fluorophore and at another end with a quencher, and thermostable DNA polymerase having 5'→3' exonuclease activity,

digesting the first probe and the second probe bound to the first base sequence and the third base sequence, by the thermostable DNA polymerase at the time of the nucleic acid amplification, and

detecting a fluorescence emitted by the first fluorophore and the second fluorophore released in digesting the first probe and the second probe, thereby assaying the amount of the product of the nucleic acid amplification.

9. (New) The method for gene expression analysis according to claim 8, wherein the first nucleotides are synthesized by introducing the first base sequence

and the second base sequence into the targeted gene using a primer, which comprises the first base sequence, which is closer to the 5' end than a fourth base sequence comprising a sequence that specifically hybridizes to the targeted gene, and the second base sequence, which is closer to the 5' end than the first base sequence, and wherein the second nucleotides are synthesized by introducing the third base sequence and the second base sequence into the targeted gene using a primer, which comprises the third base sequence, which is closer to the 5' end than the fourth base sequence comprising a sequence that specifically hybridizes to the targeted gene, and the second base sequence, which is closer to the 5' end than the first base sequence.

10. (New) The method for gene expression analysis according to claim 8, wherein the first nucleotides are cDNA comprising the first base sequence and the second base sequence introduced therein by subjecting mRNA of the targeted gene to reverse transcription using a primer which comprises the first base sequence, which is closer to the 5' end than a fourth base sequence comprising a sequence that specifically hybridizes to the targeted gene and the second base sequence, which is closer to the 5' end than the first base sequence, and wherein the second nucleotides are cDNA comprising the third base sequence and the second base sequence introduced therein by subjecting mRNA of the targeted gene to reverse transcription using a primer which comprises the third base sequence, which is closer to the 5' end than the fourth base sequence comprising a sequence that specifically hybridizes to the targeted gene and the second base sequence, which is closer to the 5' end than the third base sequence.

11. (New) The method for gene expression analysis according to claim 8, wherein the Tm values of the first probe and the second probe are substantially the same.